



## SEQUENCE LISTING

<110> SCHLEHUBER, STEFFEN

<120> MUTEINS OF THE BILIN-BINDING PROTEIN

<130> 029029-0101

<140> 09/980,862

<141> 2002-02-27

<150> PCT/DE00/01873

<151> 2000-06-08

<150> DE 199 26 068.0

<151> 1999-06-08

<160> 29

<170> PatentIn Ver. 2.1

<210> 1

<211> 1219

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
pBBP20 nucleic acid sequence

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<221> CDS

<222> (22)..(1209)

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<221> sig\_peptide

<222> (22)..(84)

<220>

<221> mat\_peptide

<222> (85)..(1209)

<223> fusion protein of bilin-binding protein, Strep-tag II  
and fragment of phage coat protein pIII

<220>

<221> misc\_feature

<222> (85)..(606)

<223> mature bilin-binding protein

<220>

<221> misc\_feature

<222> (607)..(636)

<223> Strep-tag II-affinity tag

<220>

<221> misc\_feature

<222> (637)..(639)

<223> amber stop codon

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (640)..(1209)

&lt;223&gt; amino acids 217-406 of coat protein pIII

&lt;400&gt; 1

tctagttaac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg	51
Met Lys Lys Thr Ala Ile Ala Ile Ala Val	
-20 -15	
gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac	99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp	
-10 -5 -1 1 5	
ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag	147
Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln	
10 15 20	
tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag	195
Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu	
25 30 35	
aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt	243
Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser	
40 45 50	
gtc aaa gtt tcg aac tac cac gta atc cac ggc aag gaa tac ttt att	291
Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile	
55 60 65	
gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac	339
Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr	
70 75 80 85	
cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta	387
His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu Asn Val Phe Asn Val	
90 95 100	
ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac	435
Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr	
105 110 115	
gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga	483
Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg	
120 125 130	
agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt	531
Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu	
135 140 145	
atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc	579
Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe	
150 155 160 165	
tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag	627
Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln	
170 175 180	

ttc gaa aaa tag gct ggc ggc ggc tct ggt ggt ggt tct ggc ggc ggc	675
Phe Glu Lys Gln Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly	
185 190 195	
tct gag ggt ggt ggc tct gag ggt ggc ggt tct gag ggt ggc ggc tct	723
Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser	
200 205 210	
gag gga ggc ggt tcc ggt ggt ggc tct ggt tcc ggt gat ttt gat tat	771
Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr	
215 220 225	
gaa aag atg gca aac gct aat aag ggg gct atg acc gaa aat gcc gat	819
Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp	
230 235 240 245	
gaa aac gcg cta cag tct gac gct aaa ggc aaa ctt gat tct gtc gct	867
Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala	
250 255 260	
act gat tac ggt gct gct atc gat ggt ttc att ggt gac gtt tcc ggc	915
Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly	
265 270 275	
ctt gct aat ggt aat ggt gct act ggt gat ttt gct ggc tct aat tcc	963
Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser	
280 285 290	
caa atg gct caa gtc ggt gac ggt gat aat tca cct tta atg aat aat	1011
Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn	
295 300 305	
ttc cgt caa tat tta cct tcc ctc cct caa tcg gtt gaa tgt cgc cct	1059
Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro	
310 315 320 325	
ttt gtc ttt ggc gct ggt aaa cca tat gaa ttt tct att gat tgt gac	1107
Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp	
330 335 340	
aaa ata aac tta ttc cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc	1155
Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala	
345 350 355	
acc ttt atg tat gta ttt tct acg ttt gct aac ata ctg cgt aat aag	1203
Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys	
360 365 370	
gag tct taataagctt	1219
Glu Ser	
375	

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&lt;211&gt; 64

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

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<221> modified\_base

<222> (35)..(36)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (38)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (41)..(42)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (44)..(45)

<223> a, t, c, g, other or unknown

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cgga 64

<210> 3

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

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<222> (19)..(20)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (46)..(47)

<223> a, t, c, g, other or unknown

<220>

<221> modified\_base

<222> (52)..(53)

<223> a, t, c, g, other or unknown

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ttgacactct t 71

<210> 4  
 <211> 74  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<220>  
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 <222> (33)..(34)  
 <223> a, t, c, g, other or unknown

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 <222> (42)..(43)  
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 <223> a, t, c, g, other or unknown

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<210> 5  
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 <223> a, t, c, g, other or unknown

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 <223> a, t, c, g, other or unknown

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<210> 6  
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<220>  
 <223> Description of Artificial Sequence: Synthetic primer

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<210> 7  
 <211> 37  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthetic primer

<400> 7  
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<210> 8  
 <211> 46  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligodeoxynucleotide

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<210> 9  
 <211> 793  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fragment of  
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<220>  
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 <222> (22)..(783)

<220>  
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 <222> (22)..(84)

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 <221> mat\_peptide  
 <222> (85)..(783)  
 <223> fusion protein of bilin-binding protein, Strep-Tag II  
 and albumin-binding domain

<220>  
 <221> misc\_feature  
 <222> (85)..(606)  
 <223> mature bilin-binding protein

<220>  
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 <222> (607)..(636)  
 <223> Strep-Tag II affinity tag

<220>  
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 <222> (637)..(783)  
 <223> albumin binding domain from Protein G

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 -20 -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac 99  
 Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp  
 -10 -5 -1 1 5

ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag 147  
 Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln  
 10 15 20

tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag 195  
 Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu  
 25 30 35

aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt 243  
 Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser  
 40 45 50

gtc aaa gtt tcg aac tac cac gta atc cac ggc aag gaa tac ttt att 291  
 Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile  
 55 60 65

gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac 339  
 Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr  
 70 75 80 85

cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta	387
His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu Asn Val Phe Asn Val	
90 95 100	
ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac	435
Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr	
105 110 115	
gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga	483
Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg	
120 125 130	
agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt	531
Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu	
135 140 145	
atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc	579
Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe	
150 155 160 165	
tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag	627
Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln	
170 175 180	
ttc gaa aaa cca gct agc ctg gct gaa gct aaa gtt ctg gct aac cgt	675
Phe Glu Lys Pro Ala Ser Leu Ala Glu Ala Lys Val Leu Ala Asn Arg	
185 190 195	
gaa ctg gac aaa tac ggt gtt tcc gac tac tac aaa aac ctc atc aac	723
Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asn	
200 205 210	
aac gct aaa acc gtt gaa ggt gtt aaa gct ctg atc gac gaa att ctc	771
Asn Ala Lys Thr Val Glu Gly Val Lys Ala Leu Ile Asp Glu Ile Leu	
215 220 225	
gca gca ctg ccg taataagctt	793
Ala Ala Leu Pro	
230	

&lt;210&gt; 10

&lt;211&gt; 17

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic oligodeoxynucleotide

&lt;400&gt; 10

gacggtgcct gtcccga

17



<210> 11  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligodeoxynucleotide

<400> 11  
 gactactggg gagccga

17

<210> 12  
 <211> 522  
 <212> DNA  
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Synthetic DigA  
 nucleic acid sequence

<220>  
 <221> CDS  
 <222> (1)..(522)  
 <223> mutein DigA without fusion parts

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 Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn  
 1 5 10 15

ttc gac tgg tcc cag tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac 96  
 Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr  
 20 25 30

ccc cat cac gag cgg aag tac gga aag tgc gga tgg gct gag tac act 144  
 Pro His His Glu Arg Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr  
 35 40 45

cct gaa ggc aag agt gtc aaa gtt tcg cgc tac tct gta atc cac ggc 192  
 Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly  
 50 55 60

aag gaa tac ttt tcc gaa ggt acc gcc tac cca gtt ggt gac tcc aag 240  
 Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys  
 65 70 75 80

att gga aag atc tac cac agc tac act att gga ggt gtg acc cag gag 288  
 Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu  
 85 90 95

ggt gta ttc aac gta ctc tcc act gac aac aag aac tac atc atc gga 336  
 Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly  
 100 105 110

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tac ttt tgc tcg tac gac gag gac aag aag gga cac atg gac ttg gtc 384
Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val
    115                      120                      125

tgg gtg ctc tcc aga agc atg gtc ctt act ggt gaa gcc aag acc gct 432
Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala
    130                      135                      140

gtc gag aac tac ctt atc ggc tcc cca gta gtc gac tcc cag aaa ctg 480
Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu
    145                      150                      155                      160

gta tac agt gac ttc tct gaa gcc gcc tgc aag gtc aac aat 522
Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn
    165                      170

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<210> 13
<211> 76
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic primer

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<222> (29)..(30)
<223> a, t, c, g, t, other or unknown

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<220>
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<223> a, t, c, g, t, other or unknown

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<222> (50)..(51)
<223> a, t, c, g, t, other or unknown

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<220>
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<222> (53)..(54)
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<223> a, t, c, g, t, other or unknown

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gtacggaaaag tgcgga 76

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<210> 14  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Fragment of  
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 <222> (22)..(1209)

<220>  
 <221> sig\_peptide  
 <222> (22)..(84)

<220>  
 <221> mat\_peptide  
 <222> (85)..(1209)  
 <223> fusion protein of bilin-binding protein, Strep-Tag II  
 and fragment of phage coat protein pIII, with  
 interrupted reading frame

<220>  
 <221> misc\_feature  
 <222> (85)..(606)  
 <223> mature bilin-binding protein with interrupted  
 reading frame

<220>  
 <221> misc\_feature  
 <222> (607)..(636)  
 <223> Strep-Tag II affinity tag

<220>  
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 <222> (637)..(639)  
 <223> amber stop codon

<220>  
 <221> misc\_feature  
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 <223> amino acids 217-406 of coat protein pIII

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 Met Lys Lys Thr Ala Ile Ala Ile Ala Val  
 -20 -15  
 gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac 99  
 Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp  
 -10 -5 -1 1 5

ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag	147
Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln	
10 15 20	
tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag	195
Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu	
25 30 35	
aag tac gga aat taatga tgg gct gag tac act cct gaa ggc aag agt	243
Lys Tyr Gly Asn Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser	
40 45 50	
gtc aaa gtt tcg aac tac cac gta atc cac ggc aag gaa tac ttt att	291
Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile	
55 60 65	
gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac	339
Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr	
70 75 80	
cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta	387
His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu Asn Val Phe Asn Val	
85 90 95	
ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac	435
Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr	
100 105 110 115	
gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga	483
Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg	
120 125 130	
agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt	531
Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu	
135 140 145	
atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc	579
Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe	
150 155 160	
tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag	627
Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln	
165 170 175	
ttc gaa aaa tag gct ggc ggc ggc tct ggt ggt ggt tct ggc ggc ggc	675
Phe Glu Lys Gln Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly	
180 185 190 195	
tct gag ggt ggt ggc tct gag ggt ggc ggt tct gag ggt ggc ggc tct	723
Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser	
200 205 210	
gag gga ggc ggt tcc ggt ggt ggc tct ggt tcc ggt gat ttt gat tat	771
Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr	
215 220 225	

gaa aag atg gca aac gct aat aag ggg gct atg acc gaa aat gcc gat	819
Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp	
230 235 240	
gaa aac gcg cta cag tct gac gct aaa ggc aaa ctt gat tct gtc gct	867
Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala	
245 250 255	
act gat tac ggt gct gct atc gat ggt ttc att ggt gac gtt tcc ggc	915
Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly	
260 265 270 275	
ctt gct aat ggt aat ggt gct act ggt gat ttt gct ggc tct aat tcc	963
Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser	
280 285 290	
caa atg gct caa gtc ggt gac ggt gat aat tca cct tta atg aat aat	1011
Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn	
295 300 305	
ttc cgt caa tat tta cct tcc ctg cct caa tcg gtt gaa tgt cgc cct	1059
Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro	
310 315 320	
ttt gtc ttt ggc gct ggt aaa cca tat gaa ttt tct att gat tgt gac	1107
Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp	
325 330 335	
aaa ata aac tta ttc cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc	1155
Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala	
340 345 350 355	
acc ttt atg tat gta ttt tct acg ttt gct aac ata ctg cgt aat aag	1203
Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys	
360 365 370	
gag tct taataagctt	1219
Glu Ser	

&lt;210&gt; 15

&lt;211&gt; 522

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Mutein DigA  
nucleic acid sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(522)

&lt;223&gt; mutein DigA16 without fusion parts

&lt;400&gt; 15

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Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn	
1 5 10 15	

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ttc gac tgg tcc cag tac cat ggt aaa tgg tgg cag gtc gcc gcg tac   96
Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr
                20                      25                      30

ccc gat cat att acg aag tac gga aag tgc gga tgg gct gag tac act   144
Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr
                35                      40                      45

cct gaa ggc aag agt gtc aaa gtt tcg cgc tac tct gta atc cac ggc   192
Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly
                50                      55                      60

aag gaa tac ttt tcc gaa ggt acc gcc tac cca gtt ggt gac tcc aag   240
Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys
                65                      70                      75                      80

att gga aag atc tac cac agc tac act att gga ggt gtg acc cag gag   288
Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu
                85                      90                      95

ggt gta ttc aac gta ctc tcc act gac aac aag aac tac atc atc gga   336
Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly
                100                     105                     110

tac ttt tgc tcg tac gac gag gac aag aag gga cac atg gac ttg gtc   384
Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val
                115                     120                     125

tgg gtg ctc tcc aga agc atg gtc ctt act ggt gaa gcc aag acc gct   432
Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala
                130                     135                     140

gtc gag aac tac ctt atc ggc tcc cca gta gtc gac tcc cag aaa ctg   480
Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu
                145                     150                     155                     160

gta tac agt gac ttc tct gaa gcc gcc tgc aag gtc aac aat           522
Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn
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<210> 16

<211> 1380

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
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<220>

<221> CDS

<222> (22) .. (636)

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				-20					-15							
gca	ctg	gct	ggg	ttc	gct	acc	gta	gcg	cag	gcc	gac	gtg	tac	cac	gac	99
Ala	Leu	Ala	Gly	Phe	Ala	Thr	Val	Ala	Gln	Ala	Asp	Val	Tyr	His	Asp	
	-10					-5				-1	1				5	
ggt	gcc	tgt	ccc	gaa	gtc	aag	cca	gtc	gac	aac	ttc	gac	tggt	tcc	cag	147
Gly	Ala	Cys	Pro	Glu	Val	Lys	Pro	Val	Asp	Asn	Phe	Asp	Trp	Ser	Gln	
				10					15					20		
tac	cat	ggt	aaa	tggt	tggt	gaa	gtc	gcc	aaa	tac	ccc	aac	tca	gtt	gag	195
Tyr	His	Gly	Lys	Trp	Trp	Glu	Val	Ala	Lys	Tyr	Pro	Asn	Ser	Val	Glu	
			25					30					35			
aag	tac	gga	aag	tgc	gga	tggt	gct	gag	tac	act	cct	gaa	ggc	aag	agt	243
Lys	Tyr	Gly	Lys	Cys	Gly	Trp	Ala	Glu	Tyr	Thr	Pro	Glu	Gly	Lys	Ser	
		40					45					50				
gtc	aaa	gtt	tgc	aac	tac	cac	gta	atc	cac	ggc	aag	gaa	tac	ttt	att	291
Val	Lys	Val	Ser	Asn	Tyr	His	Val	Ile	His	Gly	Lys	Glu	Tyr	Phe	Ile	
	55					60					65					
gaa	gga	act	gcc	tac	cca	gtt	ggt	gac	tcc	aag	att	gga	aag	atc	tac	339
Glu	Gly	Thr	Ala	Tyr	Pro	Val	Gly	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	
	70				75					80					85	
cac	agc	ctg	act	tac	gga	ggt	gtc	acc	aag	gag	aac	gta	ttc	aac	gta	387
His	Ser	Leu	Thr	Tyr	Gly	Gly	Val	Thr	Lys	Glu	Asn	Val	Phe	Asn	Val	
				90					95					100		
ctc	tcc	act	gac	aac	aag	aac	tac	atc	atc	gga	tac	tac	tgc	aaa	tac	435
Leu	Ser	Thr	Asp	Asn	Lys	Asn	Tyr	Ile	Ile	Gly	Tyr	Tyr	Cys	Lys	Tyr	
			105					110					115			

gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga	483
Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg	
120 125 130	
agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt	531
Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu	
135 140 145	
atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc	579
Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe	
150 155 160 165	
tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag	627
Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln	
170 175 180	
ttc gaa aaa taataagctt cgggaagatt t atg aag aaa ggt ttt atg ttg	678
Phe Glu Lys Met Lys Lys Gly Phe Met Leu	
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ttt act ttg tta gcg gcg ttt tca ggc ttt gct cag gct gat gac gcg	726
Phe Thr Leu Leu Ala Ala Phe Ser Gly Phe Ala Gln Ala Asp Asp Ala	
-10 -5 -1 1	
gca att caa caa acg tta gcc aaa atg ggc atc aaa agc agc gat att	774
Ala Ile Gln Gln Thr Leu Ala Lys Met Gly Ile Lys Ser Ser Asp Ile	
5 10 15	
cag ccc gcg cct gta gct ggc atg aag aca gtt ctg act aac agc ggc	822
Gln Pro Ala Pro Val Ala Gly Met Lys Thr Val Leu Thr Asn Ser Gly	
20 25 30 35	
gtg ttg tac atc acc gat gat ggt aaa cat atc att cag ggg cca atg	870
Val Leu Tyr Ile Thr Asp Asp Gly Lys His Ile Ile Gln Gly Pro Met	
40 45 50	
tat gac gtt agt ggc acg gct ccg gtc aat gtc acc aat aag atg ctg	918
Tyr Asp Val Ser Gly Thr Ala Pro Val Asn Val Thr Asn Lys Met Leu	
55 60 65	
tta aag cag ttg aat gcg ctt gaa aaa gag atg atc gtt tat aaa gcg	966
Leu Lys Gln Leu Asn Ala Leu Glu Lys Glu Met Ile Val Tyr Lys Ala	
70 75 80	
ccg cag gaa aaa cac gtc atc acc gtg ttt act gat att acc tgt ggt	1014
Pro Gln Glu Lys His Val Ile Thr Val Phe Thr Asp Ile Thr Cys Gly	
85 90 95	
tac tgc cac aaa ctg cat gag caa atg gca gac tac aac gcg ctg ggg	1062
Tyr Cys His Lys Leu His Glu Gln Met Ala Asp Tyr Asn Ala Leu Gly	
100 105 110 115	
atc acc gtg cgt tat ctt gct ttc ccg cgc cag ggg ctg gac agc gat	1110
Ile Thr Val Arg Tyr Leu Ala Phe Pro Arg Gln Gly Leu Asp Ser Asp	
120 125 130	



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gca gag aaa gaa atg aaa gct atc tgg tgt gcg aaa gat aaa aac aaa 1158
Ala Glu Lys Glu Met Lys Ala Ile Trp Cys Ala Lys Asp Lys Asn Lys
      135                      140                      145

gcg ttt gat gat gtg atg gca ggt aaa agc gtc gca cca gcc agt tgc 1206
Ala Phe Asp Asp Val Met Ala Gly Lys Ser Val Ala Pro Ala Ser Cys
      150                      155                      160

gac gtg gat att gcc gac cat tac gca ctt ggc gtc cag ctt ggc gtt 1254
Asp Val Asp Ile Ala Asp His Tyr Ala Leu Gly Val Gln Leu Gly Val
      165                      170                      175

agc ggt act ccg gca gtt gtg ctg agc aat ggc aca ctt gtt ccg ggt 1302
Ser Gly Thr Pro Ala Val Val Leu Ser Asn Gly Thr Leu Val Pro Gly
      180                      185                      190                      195

tac cag ccg ccg aaa gag atg aaa gaa ttc ctc gac gaa cac caa aaa 1350
Tyr Gln Pro Pro Lys Glu Met Lys Glu Phe Leu Asp Glu His Gln Lys
      200                      205                      210

atg acc agc ggt aaa taattcgcggt agctt 1380
Met Thr Ser Gly Lys
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<210> 17

<211> 2009

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
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<221> CDS

<222> (23)..(1999)

<220>

<221> sig\_peptide

<222> (23)..(85)

<220>

<221> mat\_peptide

<222> (86)..(1999)

<223> fusion protein of alkaline phosphatase, linker peptide  
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<220>

<221> misc\_feature

<222> (86)..(1435)

<223> mature part of alkaline phosphatase

<220>

<221> misc\_feature

<222> (1436)..(1447)

<223> linker peptide Pro-Pro-Ser-Ala

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<220>  
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 <222> (1970)..(1999)  
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Leu Pro Leu Leu Phe Thr Pro Val Thr Lys Ala Arg Thr Pro Glu Met	
-10 -5 -1 1 5	
cct gtt ctg gaa aac cgg gct gct cag ggc gat att act gca ccc ggc	148
Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp Ile Thr Ala Pro Gly	
10 15 20	
ggg gct cgc cgt tta acg ggt gat cag act gcc gct ctg cgt gat tct	196
Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala Ala Leu Arg Asp Ser	
25 30 35	
ctt agc gat aaa cct gca aaa aat att att ttg ctg att ggc gat ggg	244
Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu Leu Ile Gly Asp Gly	
40 45 50	
atg ggg gac tcg gaa att act gcc gca cgt aat tat gcc gaa ggt gcg	292
Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn Tyr Ala Glu Gly Ala	
55 60 65	
ggc ggc ttt ttt aaa ggt ata gat gcc tta ccg ctt acc ggg caa tac	340
Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro Leu Thr Gly Gln Tyr	
70 75 80 85	
act cac tat gcg ctg aat aaa aaa acc ggc aaa ccg gac tac gtc acc	388
Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys Pro Asp Tyr Val Thr	
90 95 100	
gac tcg gct gca tca gca acc gcc tgg tca acc ggt gtc aaa acc tat	436
Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr Gly Val Lys Thr Tyr	
105 110 115	
aac ggc gcg ctg ggc gtc gat att cac gaa aaa gat cac cca acg att	484
Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys Asp His Pro Thr Ile	
120 125 130	
ctg gaa atg gca aaa gcc gca ggt ctg gcg acc ggt aac gtt tct acc	532
Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr Gly Asn Val Ser Thr	
135 140 145	
gca gag ttg cag gat gcc acg ccc gct gcg ctg gtg gca cat gtg acc	580
Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu Val Ala His Val Thr	
150 155 160 165	

tcg cgc aaa tgc tac ggt ccg agc gcg acc agt gaa aaa tgt ccg ggt	628
Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser Glu Lys Cys Pro Gly	
170 175 180	
aac gct ctg gaa aaa ggc gga aaa gga tcg att acc gaa cag ctg ctt	676
Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile Thr Glu Gln Leu Leu	
185 190 195	
aac gct cgt gcc gac gtt acg ctt ggc ggc ggc gca aaa acc ttt gct	724
Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly Ala Lys Thr Phe Ala	
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Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys Thr Leu Arg Glu Gln	
215 220 225	
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Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp Ala Ala Ser Leu Asn	
230 235 240 245	
tcg gtg acg gaa gcg aat cag caa aaa ccc ctg ctt ggc ctg ttt gct	868
Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu Leu Gly Leu Phe Ala	
250 255 260	
gac ggc aat atg cca gtg cgc tgg cta gga ccg aaa gca acg tac cat	916
Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro Lys Ala Thr Tyr His	
265 270 275	
ggc aat atc gat aag ccc gca gtc acc tgt acg cca aat ccg caa cgt	964
Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr Pro Asn Pro Gln Arg	
280 285 290	
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Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr Asp Lys Ala Ile Glu	
295 300 305	
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Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu Gln Val Glu Gly Ala	
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tca atc gat aaa cag gat cat gct gcg aat cct tgt ggg caa att ggc	1108
Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro Cys Gly Gln Ile Gly	
330 335 340	
gag acg gtc gat ctc gat gaa gcc gta caa cgg gcg ctg gaa ttc gct	1156
Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg Ala Leu Glu Phe Ala	
345 350 355	
aaa aag gag ggt aac acg ctg gtc ata gtc acc gct gat cac gcc cac	1204
Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr Ala Asp His Ala His	
360 365 370	
gcc agc cag att gtt gcg ccg gat acc aaa gct ccg ggc ctc acc cag	1252
Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln	
375 380 385	

gcg cta aat acc aaa gat ggc gca gtg atg gtg atg agt tac ggg aac	1300
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390 395 400 405	
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Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile Ala	
410 415 420	
gcg tat ggc ccg cat gcc gcc aat gtt gtt gga ctg acc gac cag acc	1396
Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly Leu Thr Asp Gln Thr	
425 430 435	
gat ctc ttc tac acc atg aaa gcc gct ctg ggg ctg aaa ccg cct agc	1444
Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly Leu Lys Pro Pro Ser	
440 445 450	
gct gac gtg tac cac gac ggt gcc tgt ccc gaa gtc aag cca gtc gac	1492
Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp	
455 460 465	
aac ttc gac tgg tcc cag tac cat ggt aaa tgg tgg cag gtc gcc gcg	1540
Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala	
470 475 480 485	
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Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr	
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Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His	
505 510 515	
ggc aag gaa tac ttt tcc gaa ggt acc gcc tac cca gtt ggt gac tcc	1684
Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser	
520 525 530	
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Lys Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln	
535 540 545	
gag ggt gta ttc aac gta ctc tcc act gac aac aag aac tac atc atc	1780
Glu Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile	
550 555 560 565	
gga tac ttt tgc tcg tac gac gag gac aag aag gga cac atg gac ttg	1828
Gly Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu	
570 575 580	
gtc tgg gtg ctc tcc aga agc atg gtc ctt act ggt gaa gcc aag acc	1876
Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr	
585 590 595	
gct gtc gag aac tac ctt atc ggc tcc cca gta gtc gac tcc cag aaa	1924
Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys	
600 605 610	

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 Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn Ser  
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aac tgg tct cac ccg cag ttc gaa aaa taataagctt 2009  
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 630 635

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 <211> 2005  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fragment of  
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 <222> (22)..(84)

<220>  
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 <222> (85)..(1998)  
 <223> fusion protein of mutein DigA16, Strep-Tag II, linker  
 peptide Gly(5) and alkaline phosphatase

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 <222> (85)..(606)  
 <223> mutein DigA16

<220>  
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 <222> (607)..(636)  
 <223> Strep-Tag II affinity tag

<220>  
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 <222> (637)..(651)  
 <223> linker peptide Gly-Gly-Gly-Gly-Gly

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 <222> (652)..(1998)  
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Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln	
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tac cat ggt aaa tgg tgg cag gtc gcc gcg tac ccc gat cat att acg	195
Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr Pro Asp His Ile Thr	
25 30 35	
aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt	243
Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser	
40 45 50	
gtc aaa gtt tcg cgc tac tct gta atc cac ggc aag gaa tac ttt tcc	291
Val Lys Val Ser Arg Tyr Ser Val Ile His Gly Lys Glu Tyr Phe Ser	
55 60 65	
gaa ggt acc gcc tac cca gtt ggt gac tcc aag att gga aag atc tac	339
Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr	
70 75 80 85	
cac agc tac act att gga ggt gtg acc cag gag ggt gta ttc aac gta	387
His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu Gly Val Phe Asn Val	
90 95 100	
ctc tcc act gac aac aag aac tac atc atc gga tac ttt tgc tcg tac	435
Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr	
105 110 115	
gac gag gac aag aag gga cac atg gac ttg gtc tgg gtg ctc tcc aga	483
Asp Glu Asp Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg	
120 125 130	
agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt	531
Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu	
135 140 145	
atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc	579
Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe	
150 155 160 165	
tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag	627
Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln	
170 175 180	
ttc gaa aaa ggt ggc ggc ggt ggt aca cca gaa atg cct gtt ctg gaa	675
Phe Glu Lys Gly Gly Gly Gly Gly Thr Pro Glu Met Pro Val Leu Glu	
185 190 195	
aac cgg gct gct cag ggc gat att act gca ccc ggc ggt gct cgc cgt	723
Asn Arg Ala Ala Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg	
200 205 210	

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Leu Thr Gly Asp Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys	
215 220 225	
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Pro Ala Lys Asn Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser	
230 235 240 245	
gaa att act gcc gca cgt aat tat gcc gaa ggt gcg ggc ggc ttt ttt	867
Glu Ile Thr Ala Ala Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe	
250 255 260	
aaa ggt ata gat gcc tta ccg ctt acc ggg caa tac act cac tat gcg	915
Lys Gly Ile Asp Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala	
265 270 275	
ctg aat aaa aaa acc ggc aaa ccg gac tac gtc acc gac tcg gct gca	963
Leu Asn Lys Lys Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala	
280 285 290	
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Ser Ala Thr Ala Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu	
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Gly Val Asp Ile His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala	
310 315 320 325	
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Lys Ala Ala Gly Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gln	
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345 350 355	
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aaa ggc gga aaa gga tcg att acc gaa cag ctg ctt aac gct cgt gcc	1251
Lys Gly Gly Lys Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala	
375 380 385	
gac gtt acg ctt ggc ggc ggc gca aaa acc ttt gct gaa acg gca acc	1299
Asp Val Thr Leu Gly Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr	
390 395 400 405	
gct ggt gaa tgg cag gga aaa acg ctg cgt gaa cag gca cag gcg cgt	1347
Ala Gly Glu Trp Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg	
410 415 420	
ggc tat cag ttg gtg agc gat gct gcc tca ctg aat tcg gtg acg gaa	1395
Gly Tyr Gln Leu Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu	
425 430 435	

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Ala Asn Gln Gln Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met	
440 445 450	
cca gtg cgc tgg cta gga ccg aaa gca acg tac cat ggc aat atc gat	1491
Pro Val Arg Trp Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp	
455 460 465	
aag ccc gca gtc acc tgt acg cca aat ccg caa cgt aat gac agt gta	1539
Lys Pro Ala Val Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val	
470 475 480 485	
cca acc ctg gcg cag atg acc gac aaa gcc att gaa ttg ttg agt aaa	1587
Pro Thr Leu Ala Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys	
490 495 500	
aat gag aaa ggc ttt ttc ctg caa gtt gaa ggt gcg tca atc gat aaa	1635
Asn Glu Lys Gly Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys	
505 510 515	
cag gat cat gct gcg aat cct tgt ggg caa att ggc gag acg gtc gat	1683
Gln Asp His Ala Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp	
520 525 530	
ctc gat gaa gcc gta caa cgg gcg ctg gaa ttc gct aaa aag gag ggt	1731
Leu Asp Glu Ala Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly	
535 540 545	
aac acg ctg gtc ata gtc acc gct gat cac gcc cac gcc agc cag att	1779
Asn Thr Leu Val Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile	
550 555 560 565	
gtt gcg ccg gat acc aaa gct ccg ggc ctc acc cag gcg cta aat acc	1827
Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr	
570 575 580	
aaa gat ggc gca gtg atg gtg atg agt tac ggg aac tcc gaa gag gat	1875
Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly Asn Ser Glu Glu Asp	
585 590 595	
tca caa gaa cat acc ggc agt cag ttg cgt att gcg gcg tat ggc ccg	1923
Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro	
600 605 610	
cat gcc gcc aat gtt gtt gga ctg acc gac cag acc gat ctc ttc tac	1971
His Ala Ala Asn Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr	
615 620 625	
acc atg aaa gcc gct ctg ggg ctg aaa taagctt	2005
Thr Met Lys Ala Ala Leu Gly Leu Lys	
630 635	

&lt;210&gt; 19

&lt;211&gt; 396

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence



&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic pBBP20  
amino acid sequence

&lt;400&gt; 19

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Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
  -20                      -15                      -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val
  -5                      -1    1                      5                      10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp
          15                      20                      25

Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly
          30                      35                      40

Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr
          45                      50                      55

His Val Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro
          60                      65                      70                      75

Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly
          80                      85                      90

Gly Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys
          95                      100                      105

Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly
          110                      115                      120

His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly
          125                      130                      135

Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val
          140                      145                      150                      155

Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys
          160                      165                      170

Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys Lys Ala Gly
          175                      180                      185

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser
          190                      195                      200

Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly
          205                      210                      215

Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala
          220                      225                      230                      235

Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser
          240                      245                      250

Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala
          255                      260                      265

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Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly  
 270 275 280

Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly  
 285 290 295

Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro  
 300 305 310 315

Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly  
 320 325 330

Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg  
 335 340 345

Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe  
 350 355 360

Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser  
 365 370 375

<210> 20

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
 synthetic pBBP22 amino acid sequence

<400> 20

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
 -20 -15 -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val  
 -5 -1 1 5 10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp  
 15 20 25

Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly  
 30 35 40

Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr  
 45 50 55

His Val Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro  
 60 65 70 75

Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly  
 80 85 90

Gly Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys  
 95 100 105

Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly  
 110 115 120  
 His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly  
 125 130 135  
 Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val  
 140 145 150 155  
 Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys  
 160 165 170  
 Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys Pro Ala Ser  
 175 180 185  
 Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly  
 190 195 200  
 Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu  
 205 210 215  
 Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro  
 220 225 230

<210> 21

<211> 174

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Diga  
amino acid sequence

<400> 21

Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn  
 1 5 10 15  
 Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr  
 20 25 30  
 Pro His His Glu Arg Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr  
 35 40 45  
 Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly  
 50 55 60  
 Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys  
 65 70 75 80  
 Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu  
 85 90 95  
 Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly  
 100 105 110  
 Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val  
 115 120 125

Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala  
130 135 140

Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu  
145 150 155 160

Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn  
165 170

<210> 22

<211> 394

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
synthetic pBBP24 amino acid sequence

<400> 22

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
-20 -15 -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val  
-5 -1 1 5 10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp  
15 20 25

Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Asn Trp Ala  
30 35 40

Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr His Val  
45 50 55

Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro Val Gly  
60 65 70 75

Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly Gly Val  
80 85 90

Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr  
95 100 105

Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly His Gln  
110 115 120

Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala  
125 130 135

Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser  
140 145 150 155

Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn  
160 165 170

Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys Lys Ala Gly Gly Gly  
 175 180 185  
 Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly  
 190 195 200  
 Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly Gly Gly  
 205 210 215  
 Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys  
 220 225 230 235  
 Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala  
 240 245 250  
 Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp  
 255 260 265  
 Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr  
 270 275 280  
 Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly  
 285 290 295  
 Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu  
 300 305 310 315  
 Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly Lys Pro  
 320 325 330  
 Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val  
 335 340 345  
 Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr  
 350 355 360  
 Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser  
 365 370

&lt;210&gt; 23

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Mutein DigA16  
 amino acid sequence

&lt;400&gt; 23

Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn  
 1 5 10 15  
 Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr  
 20 25 30  
 Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr  
 35 40 45

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Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly
  50                      55                      60

Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys
  65                      70                      75                      80

Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu
                      85                      90                      95

Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly
                      100                      105                      110

Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val
                      115                      120                      125

Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala
                      130                      135                      140

Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu
145                      150                      155                      160

Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn
                      165                      170

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<210> 24
<211> 205
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Fragment of
       synthetic pBBP21 amino acid sequence

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<400> 24
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
  -20                      -15                      -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val
  -5                      -1    1                      5                      10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp
                      15                      20                      25

Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly
                      30                      35                      40

Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr
                      45                      50                      55

His Val Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro
  60                      65                      70                      75

Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly
                      80                      85                      90

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Gly Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys  
                   95                  100                  105

Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly  
           110                  115                  120

His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly  
       125                  130                  135

Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val  
   140                  145                  150                  155

Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys  
                   160                  165                  170

Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys  
           175                  180

<210> 25  
 <211> 236  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fragment of  
       synthetic pBBP21 amino acid sequence

<400> 25  
 Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly  
 -20                  -15                  -10                  -5

Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met  
           -1      1                  5                  10

Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys  
       15                  20                  25

Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys  
       30                  35                  40

His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val  
       45                  50                  55                  60

Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys  
           65                  70                  75

Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val  
           80                  85                  90

Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met  
       95                  100                  105

Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro  
       110                  115                  120

Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp  
   125                  130                  135                  140

Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys  
 145 150 155  
 Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala  
 160 165 170  
 Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser  
 175 180 185  
 Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu  
 190 195 200  
 Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys  
 205 210 215

<210> 26

<211> 659

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
synthetic pBBP27 amino acid sequence

<400> 26

Val Lys Gln Ser Thr Ile Ala Leu Ala Leu Leu Pro Leu Leu Phe Thr  
 -20 -15 -10  
 Pro Val Thr Lys Ala Arg Thr Pro Glu Met Pro Val Leu Glu Asn Arg  
 -5 -1 1 5 10  
 Ala Ala Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr  
 15 20 25  
 Gly Asp Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala  
 30 35 40  
 Lys Asn Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile  
 45 50 55  
 Thr Ala Ala Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly  
 60 65 70 75  
 Ile Asp Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn  
 80 85 90  
 Lys Lys Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala  
 95 100 105  
 Thr Ala Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val  
 110 115 120  
 Asp Ile His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala  
 125 130 135



Ala	Gly	Leu	Ala	Thr	Gly	Asn	Val	Ser	Thr	Ala	Glu	Leu	Gln	Asp	Ala	
140					145					150					155	
Thr	Pro	Ala	Ala	Leu	Val	Ala	His	Val	Thr	Ser	Arg	Lys	Cys	Tyr	Gly	
				160					165					170		
Pro	Ser	Ala	Thr	Ser	Glu	Lys	Cys	Pro	Gly	Asn	Ala	Leu	Glu	Lys	Gly	
			175					180					185			
Gly	Lys	Gly	Ser	Ile	Thr	Glu	Gln	Leu	Leu	Asn	Ala	Arg	Ala	Asp	Val	
	190						195					200				
Thr	Leu	Gly	Gly	Gly	Ala	Lys	Thr	Phe	Ala	Glu	Thr	Ala	Thr	Ala	Gly	
	205					210					215					
Glu	Trp	Gln	Gly	Lys	Thr	Leu	Arg	Glu	Gln	Ala	Gln	Ala	Arg	Gly	Tyr	
220					225					230					235	
Gln	Leu	Val	Ser	Asp	Ala	Ala	Ser	Leu	Asn	Ser	Val	Thr	Glu	Ala	Asn	
				240					245						250	
Gln	Gln	Lys	Pro	Leu	Leu	Gly	Leu	Phe	Ala	Asp	Gly	Asn	Met	Pro	Val	
			255					260					265			
Arg	Trp	Leu	Gly	Pro	Lys	Ala	Thr	Tyr	His	Gly	Asn	Ile	Asp	Lys	Pro	
		270					275					280				
Ala	Val	Thr	Cys	Thr	Pro	Asn	Pro	Gln	Arg	Asn	Asp	Ser	Val	Pro	Thr	
	285					290					295					
Leu	Ala	Gln	Met	Thr	Asp	Lys	Ala	Ile	Glu	Leu	Leu	Ser	Lys	Asn	Glu	
300					305					310					315	
Lys	Gly	Phe	Phe	Leu	Gln	Val	Glu	Gly	Ala	Ser	Ile	Asp	Lys	Gln	Asp	
				320					325					330		
His	Ala	Ala	Asn	Pro	Cys	Gly	Gln	Ile	Gly	Glu	Thr	Val	Asp	Leu	Asp	
			335				340						345			
Glu	Ala	Val	Gln	Arg	Ala	Leu	Glu	Phe	Ala	Lys	Lys	Glu	Gly	Asn	Thr	
		350					355					360				
Leu	Val	Ile	Val	Thr	Ala	Asp	His	Ala	His	Ala	Ser	Gln	Ile	Val	Ala	
	365					370					375					
Pro	Asp	Thr	Lys	Ala	Pro	Gly	Leu	Thr	Gln	Ala	Leu	Asn	Thr	Lys	Asp	
380					385					390					395	
Gly	Ala	Val	Met	Val	Met	Ser	Tyr	Gly	Asn	Ser	Glu	Glu	Asp	Ser	Gln	
				400					405					410		
Glu	His	Thr	Gly	Ser	Gln	Leu	Arg	Ile	Ala	Ala	Tyr	Gly	Pro	His	Ala	
			415					420					425			
Ala	Asn	Val	Val	Gly	Leu	Thr	Asp	Gln	Thr	Asp	Leu	Phe	Tyr	Thr	Met	
		430					435					440				

Lys Ala Ala Leu Gly Leu Lys Pro Pro Ser Ala Asp Val Tyr His Asp  
 445 450 455  
 Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln  
 460 465 470 475  
 Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr Pro Asp His Ile Thr  
 480 485 490  
 Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser  
 495 500 505  
 Val Lys Val Ser Arg Tyr Ser Val Ile His Gly Lys Glu Tyr Phe Ser  
 510 515 520  
 Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr  
 525 530 535  
 His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu Gly Val Phe Asn Val  
 540 545 550 555  
 Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr  
 560 565 570  
 Asp Glu Asp Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg  
 575 580 585  
 Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu  
 590 595 600  
 Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe  
 605 610 615  
 Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln  
 620 625 630 635  
 Phe Glu Lys

<210> 27

<211> 659

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of  
synthetic pBBP29 amino acid sequence

<400> 27

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala  
 -20 -15 -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val  
 -5 -1 1 5 10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp  
 15 20 25

Gln Val Ala Ala Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly  
           30                                  35                                  40

Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr  
       45                                  50                                  55

Ser Val Ile His Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro  
       60                                  65                                  70                                  75

Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly  
                                   80                                  85                                  90

Gly Val Thr Gln Glu Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys  
                                   95                                  100                                  105

Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly  
           110                                  115                                  120

His Met Asp Leu Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly  
       125                                  130                                  135

Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val  
       140                                  145                                  150                                  155

Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys  
                                   160                                  165                                  170

Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly  
                                   175                                  180                                  185

Gly Gly Thr Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly  
       190                                  195                                  200

Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr  
       205                                  210                                  215

Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile  
       220                                  225                                  230                                  235

Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg  
                                   240                                  245                                  250

Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu  
                                   255                                  260                                  265

Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly  
       270                                  275                                  280

Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser  
       285                                  290                                  295

Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu  
       300                                  305                                  310                                  315

Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala  
                                   320                                  325                                  330

Thr Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala  
 335 340 345  
 Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr  
 350 355 360  
 Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser  
 365 370 375  
 Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly  
 380 385 390 395  
 Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly  
 400 405 410  
 Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser  
 415 420 425  
 Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro  
 430 435 440  
 Leu Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly  
 445 450 455  
 Pro Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys  
 460 465 470 475  
 Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met  
 480 485 490  
 Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe  
 495 500 505  
 Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn  
 510 515 520  
 Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln  
 525 530 535  
 Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val  
 540 545 550 555  
 Thr Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys  
 560 565 570  
 Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met  
 575 580 585  
 Val Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Glu His Thr Gly  
 590 595 600  
 Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val  
 605 610 615  
 Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu  
 620 625 630 635  
 Gly Leu Lys

<210> 28  
 <211> 174  
 <212> PRT  
 <213> *Pieris brassicae*

<400> 28  
 Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn  
   1                  5                  10                  15  
 Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr  
                   20                  25                  30  
 Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr  
                   35                  40                  45  
 Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr His Val Ile His Gly  
                   50                  55                  60  
 Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys  
   65                  70                  75                  80  
 Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu  
                   85                  90                  95  
 Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly  
                   100                  105                  110  
 Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val  
                   115                  120                  125  
 Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala  
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 Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu  
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